

1/14

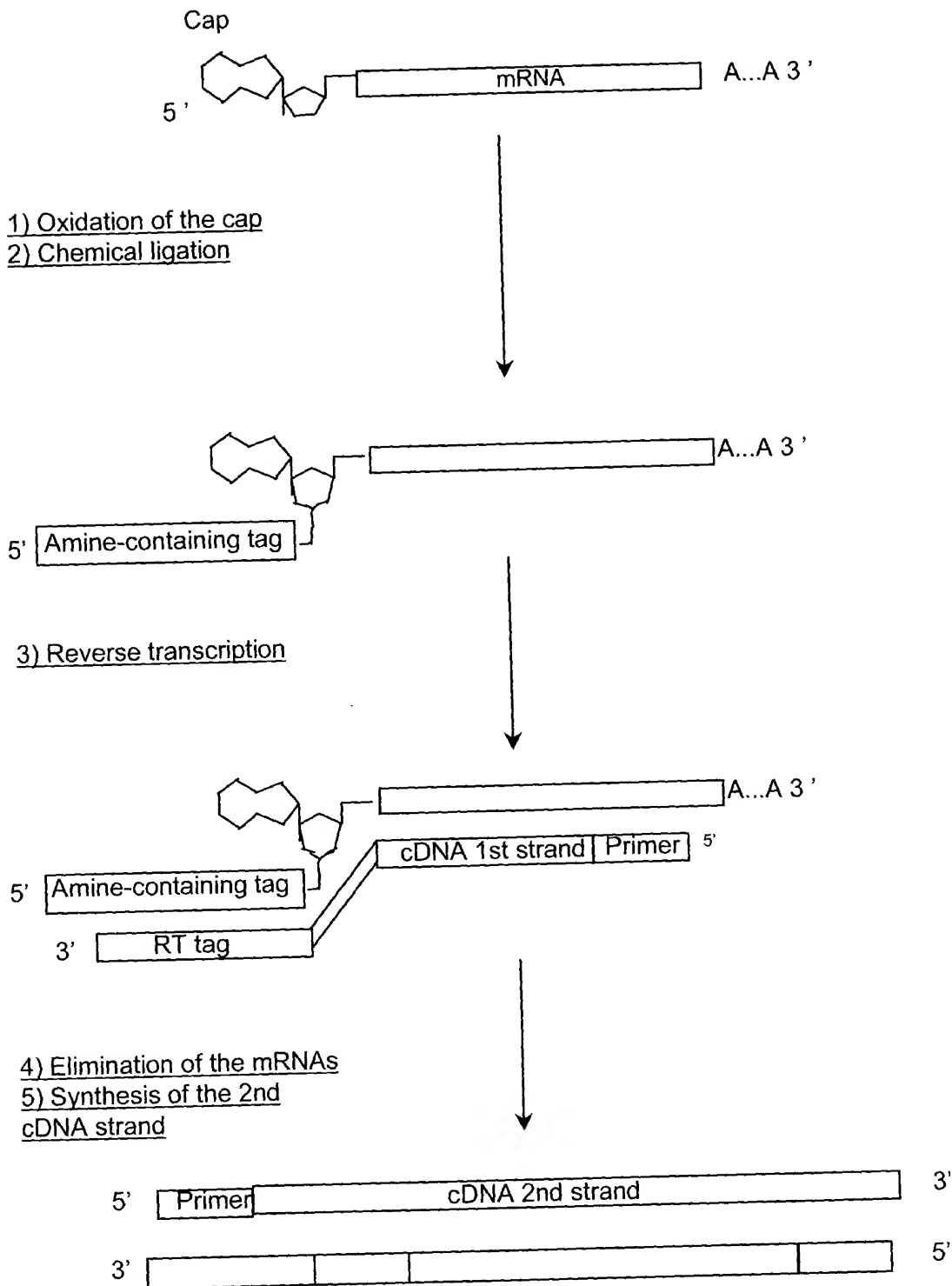


FIGURE 1

FIGURE 2

3/14

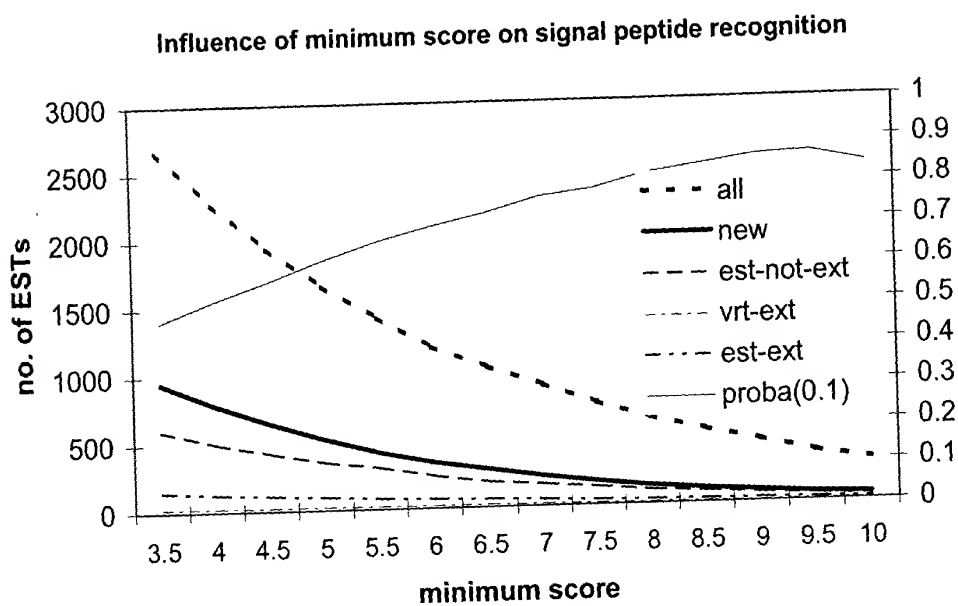


FIGURE 3

4/14

Minimum signal peptide score	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
3.5	2674	947	599	23	150
4	2278	784	499	23	126
4.5	1943	647	425	22	112
5	1657	523	353	21	96
5.5	1417	419	307	19	80
6	1190	340	238	18	68
6.5	1035	280	186	18	60
7	893	219	161	15	48
7.5	753	173	132	12	36
8	636	133	101	11	29
8.5	543	104	83	8	26
9	456	81	63	6	24
9.5	364	57	48	6	18
10	303	47	35	6	15

FIGURE 4

TOPP20"06TE0660

5/14

Tissue	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
Brain	329	131	75	3	24
Cancerous prostate	134	40	37	1	6
Cerebellum	17	9	1	0	6
Colon	21	11	4	0	0
Dystrophic muscle	41	18	8	0	1
Fetal brain	70	37	16	0	1
Fetal kidney	227	116	46	1	19
Fetal liver	13	7	2	0	0
Heart	30	15	7	0	1
Hypertrophic prostate	86	23	22	2	2
Kidney	10	7	3	0	0
Large intestine	21	8	4	0	1
Liver	23	9	6	0	0
Lung	24	12	4	0	1
Lung (cells)	57	38	6	0	4
Lymph ganglia	163	60	23	2	12
Lymphocytes	23	6	4	0	2
Muscle	33	16	6	0	4
Normal prostate	181	61	45	7	11
Ovary	90	57	12	1	2
Pancreas	48	11	6	0	1
Placenta	24	5	1	0	0
Prostate	34	16	4	0	2
Spleen	56	28	10	0	1
Substantia nigra	108	47	27	1	6
Surrenals	15	3	3	1	0
Testis	131	68	25	1	8
Thyroid	17	8	2	0	2
Umbilical cord	55	17	12	1	3
Uterus	28	15	3	0	2
Non tissue-specific	568	48	177	2	28
Total	2677	947	601	23	150

FIGURE 5

101120-061E0660

6/14

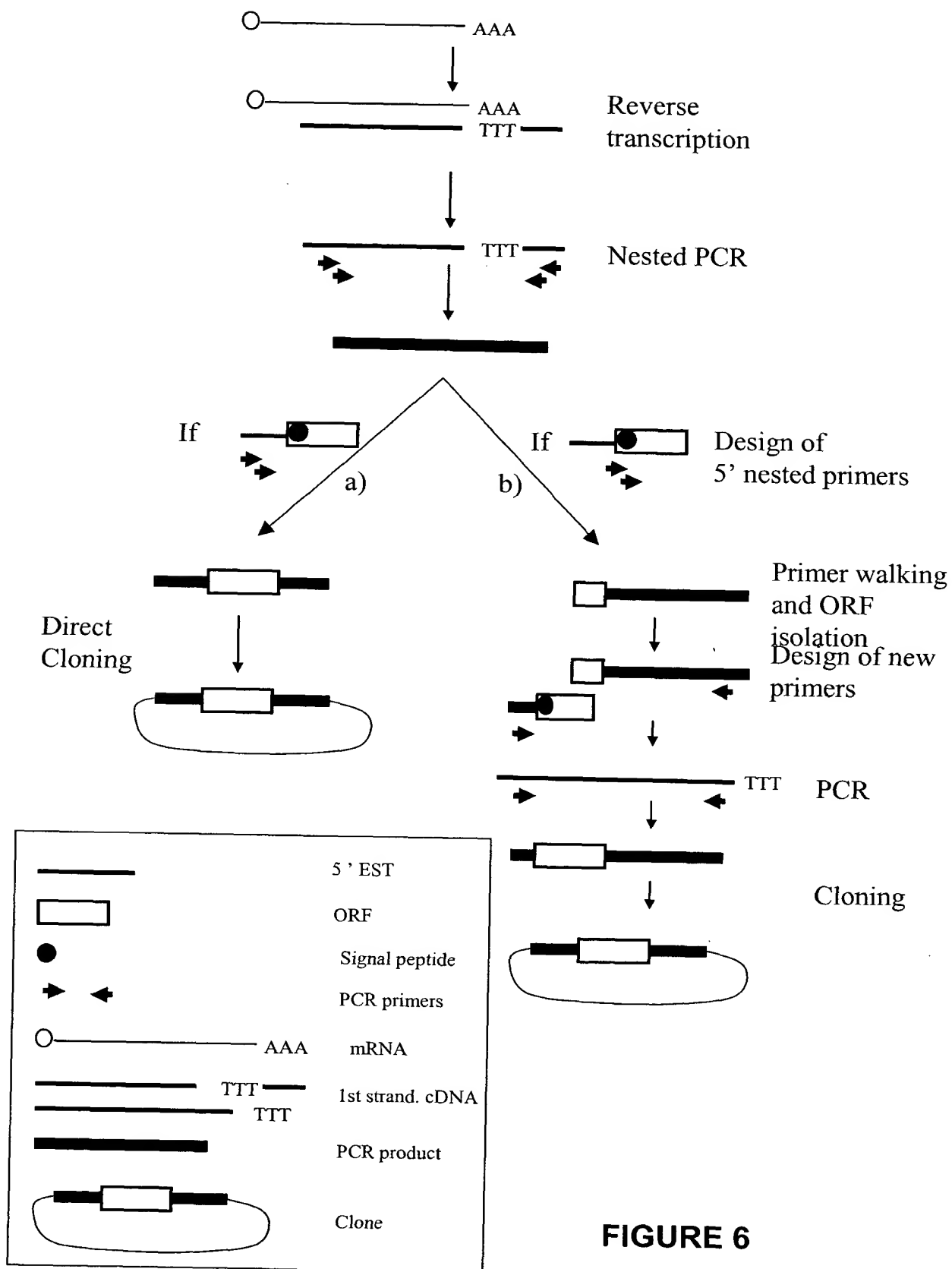
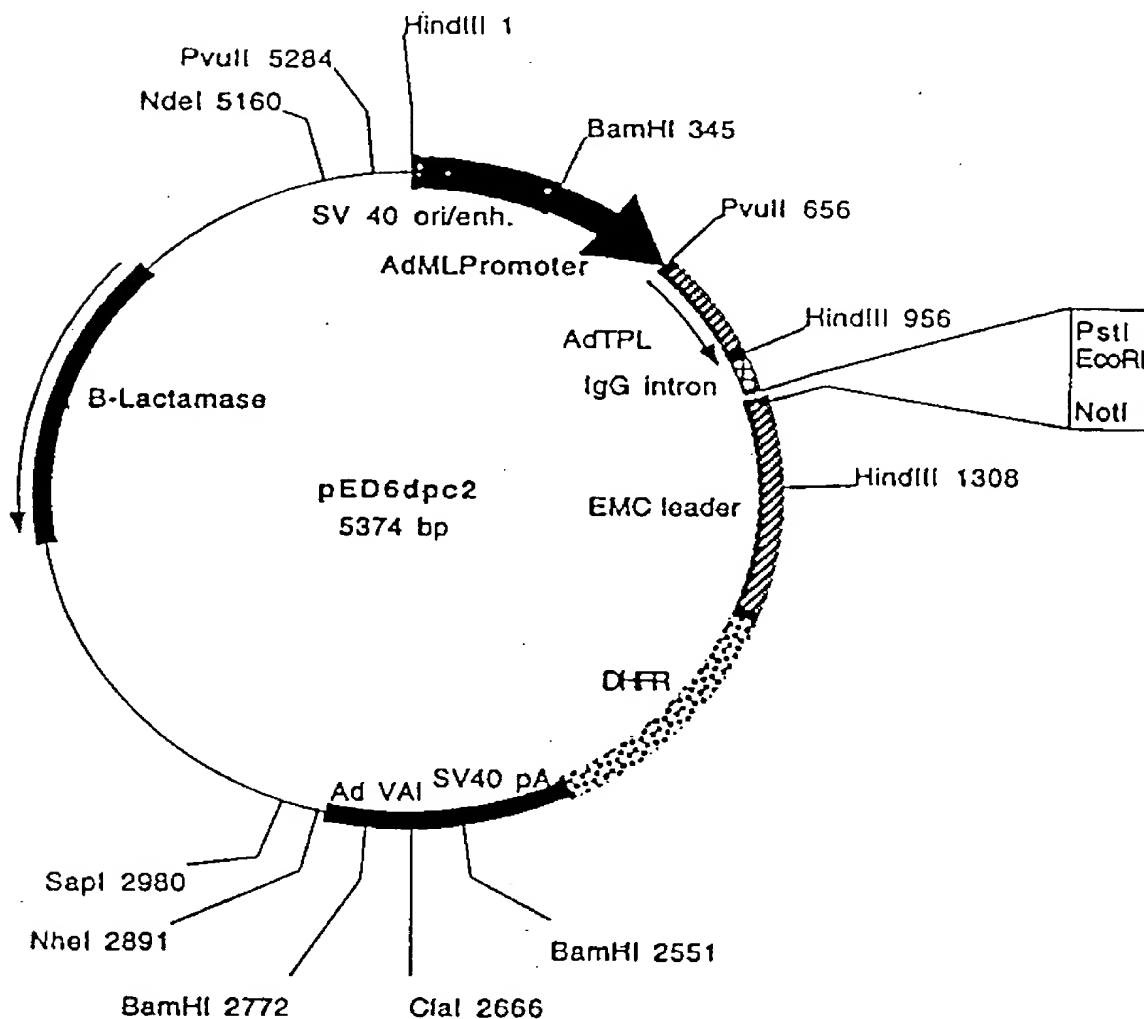


FIGURE 6

7/14



Plasmid name: pED6dpc2

Plasmid size: 5347 bp

Comments/References: pED6dpc2 is derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kaufman et al. (1991), NAR 19:4485-4490.

FIGURE 7

Description of promoters structure isolated from SignalTag 5'ESTs

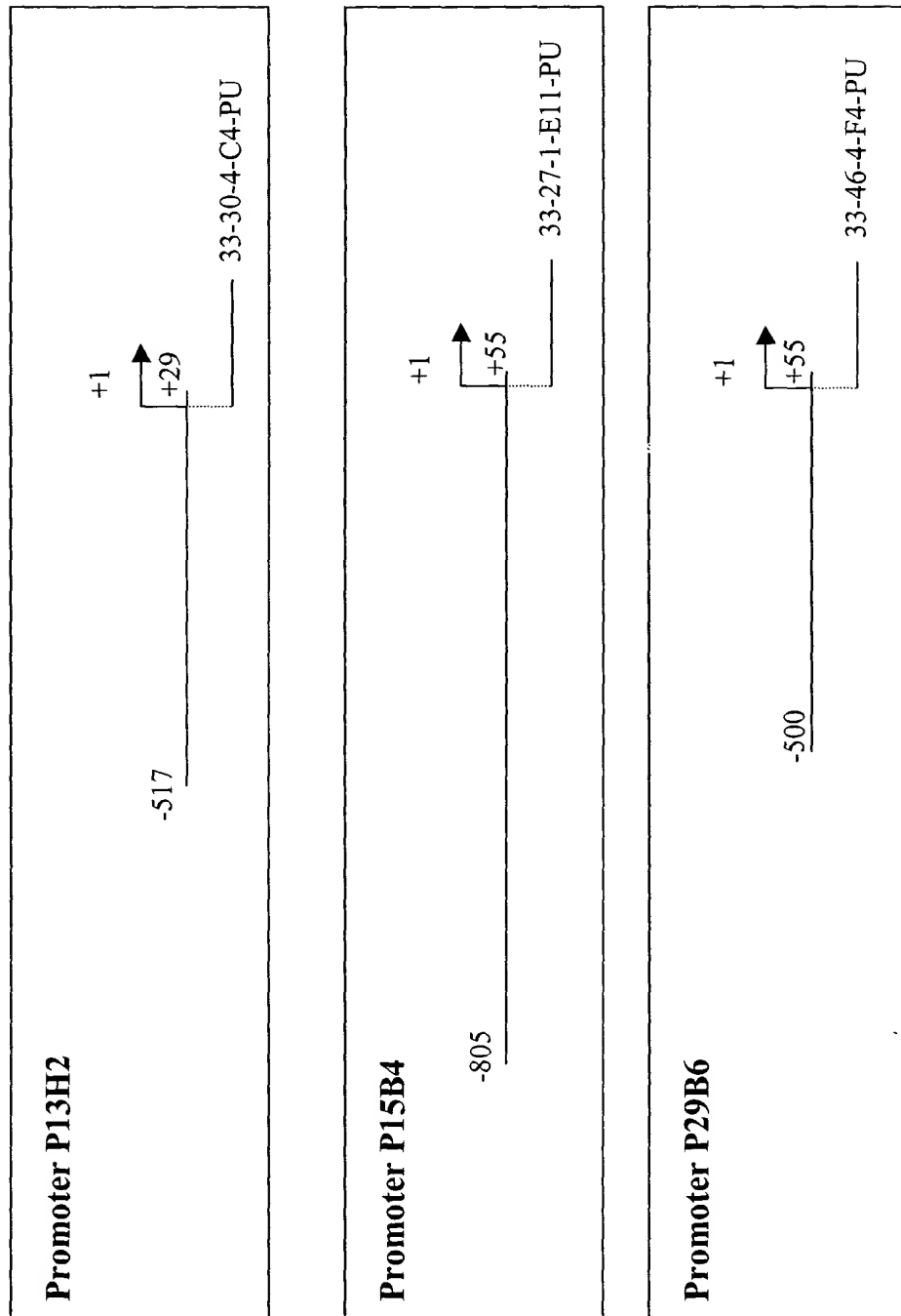


FIGURE 8

9/14

Description of Transcription Factor Binding Sites present on promoters isolated from SignalTag sequences

Promoter sequence P13H2 (546 bp):					
Matrix	Position	Orientation	Score	Length	Sequence
CMYB 01	-502	+	0.983	9	TGTCAGTTG
MYOD Q6	-501	-	0.961	10	CCCAACTGAC
S8 01	-444	-	0.960	11	AATAGAATTAG
S8 01	-425	+	0.966	11	AACTAAATTAG
DELTAEF1 01	-390	-	0.960	11	GCACACCTCAG
GATA C	-364	-	0.964	11	AGATAAATCCA
CMYB 01	-349	+	0.958	9	CTTCAGTTG
GATA1 02	-343	+	0.959	14	TTGTAGATAGGACA
GATA C	-339	+	0.953	11	AGATAGGACAT
TAL1ALPHA47 01	-235	+	0.973	16	CATAACAGATGGTAAG
TAL1BETA47 01	-235	+	0.983	16	CATAACAGATGGTAAG
TAL1BETAITF2 01	-235	+	0.978	16	CATAACAGATGGTAAG
MYOD Q6	-232	-	0.954	10	ACCATCTGTT
GATA1 04	-217	-	0.953	13	TCAAGATAAAGTA
IK1 01	-126	+	0.963	13	AGTTGGGAATTCC
IK2 01	-126	+	0.985	12	AGTTGGGAATTC
CREL 01	-123	+	0.962	10	TGGGAATTCC
GATA1 02	-96	+	0.950	14	TCAGTGATATGGCA
SRY 02	-41	-	0.951	12	TAAAACAAAACA
E2F 02	-33	+	0.957	8	TTAGCGC
MZF1 01	-5	-	0.975	8	TGAGGGGA

FIGURE 9

FIGURE 9

10/14

Promoter sequence P15B4 (861bp) :					
Matrix	Position	Orientation	Score	Length	Sequence
NFY_Q6	-748	-	0.956	11	GGACCAATCAT
MZF1_01	-738	+	0.962	8	CCTGGGGA
CMYB_01	-684	+	0.994	9	TGACCGTTG
VMYB_02	-682	-	0.985	9	TCCAACGGT
STAT_01	-673	+	0.968	9	TTCTTGAA
STAT_01	-673	-	0.951	9	TTCCAGGAA
MZF1_01	-556	-	0.956	8	TTGGGGGA
IK2_01	-451	+	0.965	12	GAATGGGATTTC
MZF1_01	-424	+	0.986	8	AGAGGGGA
SRY_02	-398	-	0.955	12	GAAAACAAAACA
MZF1_01	-216	+	0.960	8	GAAGGGGA
MYOD_Q6	-190	+	0.981	10	AGCATCTGCC
DELTAEF1_01	-176	+	0.958	11	TCCCACCTTCC
S8_01	5	-	0.992	11	GAGGCAATTAT
MZF1_01	16	-	0.986	8	AGAGGGGA

FIGURE 9 (cont)

TOTTA 06FE0600

11/14

Promoter sequence P29B6 (555 bp) :					
Matrix	Position	Orientation	Score	Length	Sequence
ARNT_01	-311	+	0.964	16	GGACTCACGTGCTGCT
NMYC_01	-309	+	0.965	12	ACTCACGTGCTG
USF_01	-309	+	0.985	12	ACTCACGTGCTG
USF_01	-309	-	0.985	12	CAGCACGTGAGT
NMYC_01	-309	-	0.956	12	CAGCACGTGAGT
MYCMAX_02	-309	-	0.972	12	CAGCACGTGAGT
USF_C	-307	+	0.997	8	TCACGTGC
USF_C	-307	-	0.991	8	GCACGTGA
MZF1_01	-292	-	0.968	8	CATGGGGA
ELK1_02	-105	+	0.963	14	CTCTCCGGAAGCCT
CETS1P54_01	-102	+	0.974	10	TCCGGAAGCC
AP1_Q4	-42	-	0.963	11	AGTGACTGAAC
AP1FJ_Q2	-42	-	0.961	11	AGTGACTGAAC
PADS_C	45	+	1.000	9	TGTGGTCTC

FIGURE 9 (cont)

FIG. 9. COMPLEMENTARY DNAS

12/14

97.8% identity in 92 aa overlap

	10	20	30	40	50	60
SEQ ID NO:120	MASLGHILVFCVGLLTM	AKAESPKEHDPFTYDYQSLQIGGLVIAGILFILGILIVLSRRC				
	10	20	30	40	50	60
SEQ ID NO:180	MAPLHHILVFCVGLLTM	AKAESPKEHDPFTYDYQSLQIGGLVIAGILFILGILIVLSRRC				
	10	20	30	40	50	60
	70	80	90			
SEQ ID NO:120	RCKFNQQQRTGEPDEEEGTFRSSIRRLSTRRR					
	70	80	90			
SEQ ID NO:180	RCKFNQQQRTGEPDEEEGTFRSSIRRLSTRRR					
	70	80	90			

FIGURE 10

FIGURE 10

Figure 1 consists of 12 sub-graphs, labeled (a) through (l), each showing the time course of a different physiological parameter over a 24-hour period. The x-axis for all graphs represents time in hours, from 0 to 24. The y-axis represents the value of the parameter. Each graph includes a solid line representing the mean value and vertical bars representing the standard error of the mean (SEM). The parameters and their approximate values at 0 and 24 hours are as follows:

- (a) HR (b/min): Starts at ~75, ends at ~70.
- (b) BP (mmHg): Starts at ~120/80, ends at ~110/70.
- (c) RR (b/min): Starts at ~15, ends at ~15.
- (d) SpO2 (%): Starts at ~98, ends at ~98.
- (e) Tcore (°C): Starts at ~37.5, ends at ~37.0.
- (f) Tsk (°C): Starts at ~36.5, ends at ~36.0.
- (g) Trect (°C): Starts at ~37.5, ends at ~37.0.
- (h) Tfeet (°C): Starts at ~36.5, ends at ~36.0.
- (i) Tleg (°C): Starts at ~36.5, ends at ~36.0.
- (j) Tarm (°C): Starts at ~36.5, ends at ~36.0.
- (k) Thead (°C): Starts at ~37.5, ends at ~37.0.
- (l) Tfinger (°C): Starts at ~36.5, ends at ~36.0.

FIGURE 11

14/14

83.4% identity in 211 aa overlap

				10	20	30
SEQ ID NO:	128			LWWFWLLWTVLILFSCCAFRHRRAKLRQ		
				:	:	:
SEQ ID NO:	182	ELCPGVNTQPYLCE	TGHCCGETGCCTYYYEL	LWWFWLLWTVLILFSCCAFRHRRAKLRQ		
		70	80	90	100	110
						120
		40	50	60	70	80
SEQ ID NO:	128	QQQRQREINLLAYHGACHGAGPFPTGSLLDLRLLS	TFKPPAYEDVVHRPGT	PPPPYT	VAP	
		:	:	:	:	:
SEQ ID NO:	182	QQQRQREINLLAYHGACHGAGPVPTGSLLDLRLLS	SAFKPPAYEDVVHPGT	PPPPYT	VGP	
		130	140	150	160	170
						180
		100	110	120	130	140
SEQ ID NO:	128	GRPLTASSEQTCCSSSSSCPAHFEGTNVEGVSSHQSAPPHQEGEPGAGVTPASTPPSCRY				
		:	:	:	:	:
SEQ ID NO:	182	GYPWTTSSECTRCSSSESSCSAHLEGTNVEGVSSQSQSALPHQEGEPRAGLSPVHIPPSCRY				
		190	200	210	220	230
						240
		160	170	180	190	200
SEQ ID NO:	128	RRLTGDSGIELCPCPASGE	GEPVKEVRVSATLPDLEDYSPCALPPESVPQIFPMGLSSE			
		:	:	:	:	:
SEQ ID NO:	182	RRLTGDSGIELCPCPDSSEGEPLKEARASASQPDLEDHSPCALPPDSVSQVPPMGLASSC				
		250	260	270	280	290
						300
SEQ ID NO:	128	GDIP				
		:				
SEQ ID NO:	182	GTSHK				

FIGURE 12